APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
10/077,130	02/15/2002	Rosana Kapeller-Libermann	MPI01-047P1RNM	2926

7590	10/25/2004

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EXAMINER
MONSHIPOURI, MARYAM

ART UNIT	PAPER NUMBER
1652	

DATE MAILED: 10/25/2004

Please find below and/or attached an Office communication concerning this application or proceeding.

	Application No.	Applicant(s)
Office Action Summary	10/077,130	KAPELLER-LIBERMANN ET AL.
	Examiner	Art Unit	
	Maryam Monshipouri	1652	

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE _3_ MONTH(S) FROM
THE MAILING DATE OF THIS COMMUNICATION.
- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed
  after SIX (6) MONTHS from the mailing date of this communication.
- If the period for reply specified above is less than thirty (30) days, a reply within the statutory minimum of thirty (30) days will be considered timely.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133).
  Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any
  earned patent term adjustment. See 37 CFR 1.704(b).

Status

1)☐ Responsive to communication(s) filed on _____.

2a)☐ This action is **FINAL**.   2b)☒ This action is non-final.

3)☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is

     closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

4)☒ Claim(s) _1-22_ is/are pending in the application.

     4a) Of the above claim(s) _8-11,13-17 and 19-22_ is/are withdrawn from consideration.

5)☐ Claim(s) _____ is/are allowed.

6)☒ Claim(s) _1-7,12 and 18_ is/are rejected.

7)☐ Claim(s) _____ is/are objected to.

8)☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

9)☐ The specification is objected to by the Examiner.

10)☐ The drawing(s) filed on _____ is/are: a)☐ accepted or b)☐ objected to by the Examiner.

     Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).

     Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).

11)☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. § 119

12)☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).

     a)☐ All   b)☐ Some * c)☐ None of:

       1.☐ Certified copies of the priority documents have been received.

       2.☐ Certified copies of the priority documents have been received in Application No. _____.

       3.☐ Copies of the certified copies of the priority documents have been received in this National Stage

         application from the International Bureau (PCT Rule 17.2(a)).

     * See the attached detailed Office action for a list of the certified copies not received.

Attachment(s)

1)☒ Notice of References Cited (PTO-892)   4)☐ Interview Summary (PTO-413)
                                                Paper No(s)/Mail Date. _____.
2)☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
3)☒ Information Disclosure Statement(s) (PTO-1449 or PTO/SB/08)   5)☐ Notice of Informal Patent Application (PTO-152)
     Paper No(s)/Mail Date _filed 7/30/04_.   6)☒ Other: attachment

Applicant's response to restriction letter filed 7/30/2004 is acknowledged.

Applicant elected Group II invention directed to claims 1-7, 12 and 18 and SEQ ID NO:5

encoding sequences only, without traverse. Claims 8-11, 13-17 and 19-22 are

withdrawn as drawn to non-elected invention.

DETAILED ACTION

Claims 1-7, 12 and 18 (directed to sequences encoding SEQ ID NO:5 only) are

under examination on the merits.

Claim Objections

Claims 1-7, 12 and 18 are objected to because of the following informalities: said

claims recite both elected (SEQ ID NO:4 and 6) as well as non-elected sequences

(SEQ ID NO: 1 and 3). Applicant is advised to delete the non-elected sequences from

the elected claims. Appropriate correction is required.

Claim Rejections - 35 USC § 112

The following is a quotation of the second paragraph of 35 U.S.C. 112:

> The specification shall conclude with one or more claims particularly pointing out and distinctly
> claiming the subject matter which the applicant regards as his invention.

Claims 1-7, 12 and 18 are rejected under 35 U.S.C. 112, second paragraph, as

being indefinite for failing to particularly point out and distinctly claim the subject matter

which applicant regards as the invention. The term "stringent conditions" in claim 1 (and

its dependent claims 2-7 and 18), and claim 12 is unclear. Applicant has not defined this

term explicitly, in the specification. In page 17 of the disclosure, many examples of

stringent conditions are recited but the exact salt and temperature conditions that

correspond to said term are not identified. Applicant may overcome this rejection by

recitation of exact salt and temperature conditions used for hybridization (based in the

support provided in the specification) into claims 1 and 12. Currently claims 2-7 are

merely rejected for depending from a rejected base claim.

Claims 1-7, 12 and 18 are rejected under 35 U.S.C. 112, second paragraph, as

being indefinite for failing to particularly point out and distinctly claim the subject matter

which applicant regards as the invention. The term "naturally occurring allelic variant" in

claim 1 (and its dependent claims 2-7 and 18) and claim 12 is unclear. Applicant in

pages 26-27 of the disclosure has provided a definition for said term but said definition

is unclear. For example, in page 26 of the disclosure applicant defines allelic variants

as both functional and non-functional. The functional variants according to applicant,

must have only conservative substitution of one or <u>more</u> amino acids of SEQ ID NO:5 in

<u>non-critical</u> regions of SEQ ID NO:5. However, it is not clear what number constitutes

the term "more" and what region constitutes "non-critical". The latter term remains

puzzling in defining non-functional variants as well.

The following is a quotation of the first paragraph of 35 U.S.C. 112:

> The specification shall contain a written description of the invention, and of the manner and process of making and using it, in such full, clear, concise, and exact terms as to enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the same and shall set forth the best mode contemplated by the inventor of carrying out his invention.

Claims 1-7, 12 and 18 are rejected under 35 U.S.C. 112, first paragraph,

because the specification, while being enabling for isolated DNA sequences encoding

SEQ ID NO:5, does not reasonably provide enablement for any of the following:

- isolated DNA molecules comprising DNA sequences which are at least 85%
  identical to SEQ ID NO:4 and 6 with no function (see base claims 1 and 12),

- Isolated DNA molecules comprising a fragment of at least 300 nucleotides of SEQ ID NO:4 and 6 with no function,

- Isolated DNA molecules encoding a fragment comprising at least 15 contiguous amino acids of SEQ ID NO :5 with no function, and

- Isolated DNA molecules encoding a naturally occurring allelic variant of SEQ ID NO:5, wherein the nucleic acid molecules hybridize to SEQ ID NO:4 or 6 or complements thereof, under stringent conditions, with no function.

The specification fails to teach which residues in the above listed DNA molecules must be retained such that said DNA molecules encode products with kinase function. No examples of such sequences are provided either. Current state of the art indicates that any DNA sequence that: (a) has 85% identity, (b) comprises 300 nucleotides of a sequence encoding a full-length polypeptide or encodes (c) a fragment of at least 15 amino acids of a full-length polypeptide or (d) a naturally occurring allelic variant of said full-length polypeptide is not necessarily going to encode a product with kinase activity.

Therefore due to lack of sufficient teachings and examples provided in the specification and due to unpredictability of prior art as to which residues in above mentioned DNA sequences must be retained such that said DNA sequences encode products that have kinase function one of skill in the art has to go through the burden of undue experimentation in order to screen for those sequences that are supported by the specification and as such claims 1 and 12 go beyond the scope of the disclosure. Claims 2-7 and 18 are rejected merely for depending from rejected base claim 1.

Claims 1, 2-7, 12 and 18 are rejected under 35 U.S.C. 112, first paragraph, as failing to comply with the written description requirement. The claim(s) contains subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention. Claims 1 (and its dependent claims 3-7) and 12 are directed to **genera** of DNA sequences that are not adequately described in the specification.

These claims are directed to the following genera:

- A genus of DNA molecules comprising DNA sequences which are at least 85% identical to SEQ ID NO:4 and 6 with no function (see base claims 1 and 12).

- A genus of DNA molecules comprising a fragment of at least 300 nucleotides of SEQ ID NO:4 and 6 with no function.

- A genus of DNA molecules encoding a fragment comprising at least 15 contiguous amino acids of SEQ ID NO :5 with no function.

- A genus of DNA molecules encoding a naturally occurring allelic variant of SEQ ID NO:5, wherein the nucleic acid molecules hybridize to SEQ ID NO:4 or 6 or complements thereof under stringent conditions, with no function.

The specification does not contain any disclosure of the function of all DNA sequences that are listed above. The genera of cDNAs that comprise these above cDNA molecules is a large variable genera with the potentiality of encoding many

different proteins. Therefore, many functionally unrelated DNAs are encompassed within the scope of these claims, including partial DNA sequences. The specification discloses only **a single species** (DNA sequences encoding SEQ ID NO:5) for each claimed genus which is insufficient to put one of skill in the art in possession of the attributes and features of all species within the claimed genus. Therefore, one skilled in the art cannot reasonably conclude that the applicant had possession of the claimed invention at the time the instant application was filed.

Applicant is further reminded that the above listed genera are further subject to written description rejection because of lack of adequate structural information. For example, the specification does not provide enough information about the DNA sequences that have 85% identity to SEQ ID NO:4 or 6. In other words the specification does not teach which residues in which region of SEQ ID NO:4 and 6 may be mutated such that they are still capable of encoding products with kinase function. Similarly, in claim 1 (b) and (d) and claim 12 (b) the disclosure is silent as to what the other residues of claimed DNA sequences must be such that said DNA sequences can still encode products with kinase function. With respect to naturally occurring allelic variants in claim 1(e) and 12 (c) again the lack of structural information persists. This is because as explained above, the definition of allelic variants in terms of structure is unclear. Thus, by reading the information provided about the genus of "allelic variants" in the disclosure one of skill in the art finds neither adequate structural nor adequate functional information (see specially non-functional variants), rendering claim 1 (and its dependent claims 3-7 and 18) and claim 12 even more subject to 112 first rejection.

Applicant is referred to the revised interim guidelines concerning compliance with

the written description requirement of U.S.C. 112, first paragraph, published in the

Official Gazette and also available at www.uspto.gov.

Claim Rejections - 35 USC § 102

The following is a quotation of the appropriate paragraphs of 35 U.S.C. 102 that

form the basis for the rejections under this section made in this Office action:

A person shall be entitled to a patent unless –

(e) the invention was described in (1) an application for patent, published under section 122(b), by another filed in the United States before the invention by the applicant for patent or (2) a patent granted on an application for patent by another filed in the United States before the invention by the applicant for patent, except that an international application filed under the treaty defined in section 351(a) shall have the effects for purposes of this subsection of an application filed in the United States only if the international application designated the United States and was published under Article 21(2) of such treaty in the English language.

Claims 1, 3-7, 12 and 18 are rejected under 35 U.S.C. 102(e) as being

anticipated by Wei et al. (U.S. Patent No. 6,482,624, issued Nov. 2002, cited in the

IDS). Wei teaches a DNA sequence (see its SEQ ID NO:1) that encodes a polypeptide

comprising at least 15 contiguous amino acids of SEQ ID NO:5 (see the attached amino

acid alignment for residues matching residues 6356-7135 of SEQ ID NO:5). Wei also

teaches (see columns 24-25) and claims vectors and hosts comprising its DNA

sequences and methods of expressing its DNA sequence, anticipating claims 3-7 and

12. In column 29, Wei teaches about kits comprising its DNA sequences for detecting a

kinase encoding nucleic acids in a biological sample, anticipating claim 18.

Claims 1, 3-7, 12 and 18 are rejected under 35 U.S.C. 102(e) as being

anticipated by Zeng et al. (US20030108533June 2003). Zeng teaches about a DNA

sequence (see its SEQ ID NO:5) that encodes a polypeptide comprising at least 15

contiguous amino acids of SEQ ID NO:5 of this invention (see the attached amino acid

alignment for residues matching residues 5373-7968 of SEQ ID NO:5). Zeng also

teaches (see page 2, column 1) and claims vectors and hosts comprising its DNA

sequences and methods of expressing its DNA sequence anticipating claims 3-7 and

12. In page 2, column 2, Zeng teaches about kits comprising its DNA sequences for

detecting a kinase encoding nucleic acids in a biological sample, anticipating claim 18.

No claims are allowed.

ALLOWABLE SUBJECT MATTER

Isolated DNA sequences encoding SEQ ID NO:5 or comprising SEQ ID

NO:4 or 6 are free of prior art. Further, the prior art does not teach or suggest

preparing such specific sequences.

Any inquiry concerning this communication or earlier communications from the

examiner should be directed to Maryam Monshipouri whose telephone number is (571)

272-0932. The examiner can normally be reached on 7:00 a.m to 4:30 p.m. except for

alternate Mondays.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's

supervisor, Ponnanthapu Achutamurthy can be reached on (571) 272-0928. The fax

phone number for the organization where this application or proceeding is assigned is

703-872-9306.

Information regarding the status of an application may be obtained from the

Patent Application Information Retrieval (PAIR) system. Status information for

published applications may be obtained from either Private PAIR or Public PAIR.
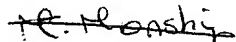
Status information for unpublished applications is available through Private PAIR only.

For more information about the PAIR system, see http://pair-direct.uspto.gov. Should

you have questions on access to the Private PAIR system, contact the Electronic

Business Center (EBC) at 866-217-9197 (toll-free).

Maryam Monshipouri Ph.D.

Primary Examiner

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Db   2521 IMLSAEYPVSSEGARDLQRGLRKGLVRLSRCYAGLSGGAVAFLRSTLCAQPWGRPCASSC 2580
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Qy   7919 LQCPWLTEEGPACSRPAPVTFPTARLRVFVRNREKRRALLYKRHNLAQVR 7968
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db   2581 LQCPWLTEEGPACSRPAPVTFPTARLRVFVRNREKRRALLYKRHNLAQVR 2630
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RESULT 5
US-10-307-019-6
; Sequence 6, Application US/10307019
; Publication No. US20030108533A1
GENERAL INFORMATION:
;   APPLICANT: Zeng, Wenlin
;   APPLICANT: Stanton, Lawrence
;   APPLICANT: SCIOS, INC.
;   TITLE OF INVENTION: MEDIATORS OF SIGNAL TRANSDUCTION
;   FILE REFERENCE: SCIOS.021DV1
;   CURRENT APPLICATION NUMBER: US/10/307,019
;   CURRENT FILING DATE: 2002-11-26
;   PRIOR APPLICATION NUMBER: 09/548,473
;   PRIOR FILING DATE: 2000-04-13
;   PRIOR APPLICATION NUMBER: 60/129,552
;   PRIOR FILING DATE: 1999-04-16
;   NUMBER OF SEQ ID NOS: 9
;   SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
;   LENGTH: 2596
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-307-019-6

Query Match   32.8%; Score 13528; DB 14; Length 2596;
Best Local Similarity   100.0%; Pred. No. 0;
Matches 2595; Conservative   0; Mismatches   1; Indels   0; Gaps   0;

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Qy   5493 AISAQGLETASFADLGGQRKEPLAAKEALGHLSLAEVGTEBFLQKLTSQITEMVSAKIT 5552
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Db    121 AISAQGLETASFADLGGQRKEPLAAKEALGHLSLAEVGTEBFLQKLTSQITEMVSAKIT 180

Qy   5553 QAKLQVPGGDSDEDSKTPSASPRHGRSRPSSIQESSSESEDGDARGEIFDIYVVTADYL 5612
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Db    181 QAKLQVPGGDSDEDSKTPSASPRHGRSRPSSIQESSSESEDGDARGEIFDIYVVTADYL 240

Qy   5613 PLGAEQDAITLREGQVEVLDAAHPLRWLVRTKPTKSSPSRQGWVSPAYLDRRLKLSPEW 5672
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Db    241 PLGAEQDAITLREGQVEVLDAAHPLRWLVRTKPTKSSPSRQGWVSPAYLDRRLKLSPEW 300

Qy   5673 GAEAPFPGEAVSEDEYKARLSSVIQELLSSEQAFVEELQPLQSHHLQHLERCPHVPIA 5732
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Qy   5733 VAGQKAVIFRNVRDIGRFHSSFLQELQQCDTDDDVAMCFIKNQAAFEQYLEFLVGRVQAE 5792
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Db    361 VAGQKAVIFRNVRDIGRFHSSFLQELQQCDTDDDVAMCFIKNQAAFEQYLEFLVGRVQAE 420

Qy   5793 SVVVSTAIQEFYKKYAEEALLAGDPSQPPPPLQHYLEQPVERVQRYQALLKELIRNKAR 5852
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Qy   5853 NRQNCALLEQAYAVVSALPQRAENKLHVSLMENYPGTLEALGEPIRQGHFIVWEGAPGAR 5912
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Qy   6899 RHLLKGGYIAGALPGLREPLMEHRVLEEEAAREQATLLAKAPSFETALRLPASGTHLAP 6958
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Qy   6959 GHSHSLEHDSPSTPRPSSEACGEAQRLPSAPSGGAPIRDMGHPQGSKQLPSTGGHPGTAQ 7018
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Qy   7019 PERPSPDSPWGQPAPFCHPKQGSAPQEGCSPHPAVAPCPPGSFPPGSCKEAPIVPSSPFL 7078
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Qy   7139 GTEPGPSLDAEGWTQEAEDLSDSTPTLQRPQEQATMRKFSLGGRGGYAGVAGYGTPAFGG 7198
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Qy   7199 DAGGMLGQGPMWARIAWAVSQSEEEEQEEARAESQSEEQQEARAESPLPQVSARPVPEVG 7258
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Qy   7259 RAPTRSSPEPTPWEDIGQVSLVQIRDLSGDAERAADTISLDISEVDPAYLNLSDLYDIKYL 7318
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   7319 PFEFMIFRKVPKSAQPEPPSPMABEELAEFPEPTWPWPGELGPHAGLEITEBESEDVDALL 7378
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Qy   7379 AEAAVGRKRKWSSPSRSLFHFPGRHLPLDEPAELGLRERVKASVEHISRILKGRPEGLEK 7438
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Qy   7439 EGPPRKKPGLASFRLSGLKSWDRAPTFLRELSDETVVLGQSVTLACQVSAQPAQATWSK 7498
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Qy   7559 SSPCPDIGEVYADGVLLVWKPVESYGPVTYIVQCSLEGGSWTTLASDIFDCCYLTSKLSR 7618
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Qy   7619 GGTYTFRTACVSKAGMGPYSSPSEQVLLGGPSHLASEEESQGRSAQPLPSTKTFAFQTQI 7678
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Db   2281 GGTYTFRTACVSKAGMGPYSSPSEQVLLGGPSHLASEEESQGRSAQPLPSTKTFAFQTQI 2340

Qy   7679 QRGRFSVVRQCWEKASGRALAAKIIPYHPDKTAVLREYEALKGLRHPHLAQLHAAYLSP 7738
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Qy   7739 RHLVLILELCSGPELLPCLAERASYSESEVKDYLWQMLSATQYLHNQHILHLDLRSENMI 7798
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Qy   7799 ITEYNLLKVVDLGNAQSISQEKVLPSDKFKDYLETMAPELLEGGQGAVPQTDIWAIGVTAF 7858
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Qy   7859 IMLSAEYPVSSEGARDLQRGLRKGLVRLSRCYAGLSGGAVAFLRSTLCAQPWGRPCASSC 7918
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Db    541 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db    601 QEREDSVRKYLLQARTAIIKSSWVKEICGIQQRLALPVWRPPDFEEELADCTAELGETVK   660
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Qy   6033 QEREDSVRKYLLQARTAIIKSSWVKEICGIQQRLALPVWRPPDFEEELADCTAELGETVK  6092

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Qy   6153 AGNCSTLGKILVQVPPRFVNKVRASPFVEGEDAQFTCTIEGAPYPQIRWYKDGALLTTGN  6212

Db    781 KFQTLSEPRSGLLVLVIRAASKEDLGLYECELVNRLGSARASAELRIQSPMLQAQEQCHR   840
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Qy   6213 KFQTLSEPRSGLLVLVIRAASKEDLGLYECELVNRLGSARASAELRIQSPMLQAQEQCHR  6272

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Qy   6333 VTGTSEAPAVPPRVPQPLLHEGPEQPEAIARAQEWTVPIRMEGAAWPGAGTGELLWDVH   6392

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Qy   6393 SHVVRETTQRTYTYQAIDTHTARPPSMQVTIEDVQAQTGGTAQFEAIIEGDPQPSVTWYK  6452

Db   1021 DSVQLVDSTRLSQQQEGTTYSLVLRHVASKDAGVYTCLAQNTGGQVLCKAELLVLGGDNE  1080
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Qy   6453 DSVQLVDSTRLSQQQEGTTYSLVLRHVASKDAGVYTCLAQNTGGQVLCKAELLVLGGDNE  6512

Db   1081 PDSEKQSHRRKLHSFYEVKEEIGRGVFGFVKRVQHKGNKILCAAKFIPLRSRTRAQAYRE  1140
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Qy   6513 PDSEKQSHRRKLHSFYEVKEEIGRGVFGFVKRVQHKGNKILCAAKFIPLRSRTRAQAYRE  6572

Db   1141 RDIIAALSHPLVTGLLDQFETRKTLILIELCSSEELLDRLYRKGVVTEAEVKVYIQQLV   1200
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Qy   6573 RDIIAALSHPLVTGLLDQFETRKTLILIELCSSEELLDRLYRKGVVTEAEVKVYIQQLV   6632

Db   1201 EGLHYLHSHGVLHLDIKPSNILMVHPAREDIKICDFGFAQNITPAELQFSQYGSPEFVSP  1260
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Qy   6693 EIIQQNPVSEASDIWAMGVISYLSLTCSSPFAGESDRATLLNVLEGRVSWSSPMAAHLSE  6752

Db   1321 DAKDFIKATLQRAPQARPSAAQCLSHPWFLKSMPAEEAHFINTKQLKFLLARSRWQRSLM  1380
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Qy   6753 DAKDFIKATLQRAPQARPSAAQCLSHPWFLKSMPAEEAHFINTKQLKFLLARSRWQRSLM  6812

Db   1381 SYKSILVMRSIPELLRGPPDSSLGVARHLCRDTGGSSSSSSDNELAPFARAKSLPPS    1440
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Qy   6813 SYKSILVMRSIPELLRGPPDSSLGVARHLCRDTGGSSSSSSDNELAPFARAKSLPPS    6872

Db   1441 PVTHSPLLHPRGFLRPSASLPEEAEASRSTEAPAPPASPEGAGPPAAQCVPRHSVIRS   1500
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Qy   7233 QSEEQQEARAESPLPQVSARPVPEVGRAPTRSSPEPTPWEDIGQVSLVQIRDLSGDAEAA  7292

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Qy   7293 DTISLDISEVDPAYLNLSDLYDIKLPFEMIFRKVPKSAQPEPPSPMAEEELAEFPEPT   7352

Db   1921 DTISLDISEVDPAYLNLSDLYDIKYLPFEFMIFRKVPKSAQPEPPSPMAEEELAEFPEPT  1980
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Qy   7353 WPWPGELGPHAGLEITEESEDVDALLAEAAVGRKRKWSSPSRSLFHFPGRHLPLDEPAEL  7412

Db   1981 WPWPGELGPHAGLEITEESEDVDALLAEAAVGRKRKWSSPSRSLFHFPGRHLPLDEPAEL  2040
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Qy   7653 ASEEESQGRSAQPLPSTKTFAFQTQIORGRFSVVRQCWEKASGRALAAKIIPYHPKDKTA  7712

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Qy   7953 KRRALLYKRHNLAQVR  7968

Db   2581 KRRALLYKRHNLAQVR  2596
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                    GenCore version 5.1.6
            Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on:     September 13, 2004, 11:16:23 ; Search time 92 Seconds
                              (without alignments)
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Perfect score: 41273
Sequence:   1 MDQPQFSGAPRFLTRPKAFV.........RNREKRRALLYXRHNLAQVR 7968

Scoring table:  BLOSUM62
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Searched:   389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters:        389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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SUMMARIES

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1	8423	20.4	1665	4	US-09-858-664A-2	Sequence 2, Appli
2	8423	20.4	1665	4	US-10-274-978-2	Sequence 2, Appli
3	1173	2.8	846	4	US-09-858-664A-3	Sequence 3, Appli
4	1173	2.8	846	4	US-10-274-978-4	Sequence 4, Appli
5	909.5	2.2	549	4	US-09-858-664A-5	Sequence 5, Appli
6	909.5	2.2	549	4	US-10-274-978-6	Sequence 6, Appli
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8	592.5	1.4	414	4	US-09-858-664A-13	Sequence 13, Appli
9	592.5	1.4	414	4	US-10-274-978-14	Sequence 14, Appli
10	531	1.3	279	4	US-09-858-664A-4	Sequence 4, Appli
11	531	1.3	279	4	US-10-274-978-5	Sequence 5, Appli
12	521	1.3	298	4	US-09-858-664A-17	Sequence 17, Appli
13	521	1.3	298	4	US-10-274-978-18	Sequence 18, Appli
14	511.5	1.2	508	4	US-09-858-664A-18	Sequence 18, Appli
15	511.5	1.2	508	4	US-10-274-978-19	Sequence 19, Appli
16	504	1.2	250	4	US-09-858-664A-6	Sequence 6, Appli
17	504	1.2	250	4	US-10-274-978-7	Sequence 7, Appli
18	489	1.2	448	2	US-09-159-385-2	Sequence 2, Appli
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21	472.5	1.1	260	2	US-07-857-224B-23	Sequence 23, Appli
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ALIGNMENTS

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RESULT 1
US-09-858-664A-2
; Sequence 2, Application US/09858664A
; Patent No. 6482624
; GENERAL INFORMATION:
;  APPLICANT: WEI, Ming-Hui, et al.
;  TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
;  TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
;  TITLE OF INVENTION: THEREOF
;  FILE REFERENCE: CL00927-CIP
;  CURRENT APPLICATION NUMBER: US/09/858,664A
;  CURRENT FILING DATE: 2001-05-17
;  PRIOR APPLICATION NUMBER: 09/711,134
;  PRIOR FILING DATE: 2000-11-11
;  NUMBER OF SEQ ID NOS: 33
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
;  LENGTH: 1665
;  TYPE: PRT
;  ORGANISM: Homo sapiens
US-09-858-664A-2

Query Match             20.4%;  Score 8423;  DB 4;  Length 1665;
Best Local Similarity   99.9%;  Pred. No. 0;
Matches 1612;  Conservative  0;  Mismatches  1;  Indels  0;  Gaps  0;

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Qy   7316 KYLPFEFMIFRKVPKSAQPEPSPNAEEELAEFPEPTWPWGELGPHAGLEITEESEDVD 7375
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Db   1013 KYLPFEFMIFRKVPKSAQPEPSPNAEEELAEFPEPTWPWGELGPHAGLEITEESEDVD 1072

Qy   7376 ALLAEAAVGRKRKRKWSSPSRSLFHFPGRHLPLDEPAELGLRERVKASVEHISRILKGRPEG 7435
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1073 ALLAEAAVGRKRKRKWSSPSRSLFHFPGRHLPLDEPAELGLRERVKASVEHISRILKGRPEG 1132

Qy   7436 LEKEGPPRKKPGLASFRLSGLKSWDRAPTFLRELSDETVVLGQSVTLACQVSAQPAAQAT 7495
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1133 LEKEGPPRKKPGLASFRLSGLKSWDRAPTFLRELSDETVVLGQSVTLACQVSAQPAAQAT 1192

Qy   7496 WSKDGAPLESSSRVLISATLKNFQLLTILVVAEDLGVYTCSVSNALGTVTTTGVLRKAE 7555
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1193 WSKDGAPLESSSRVLISATLKNFQLLTILVVAEDLGVYTCSVSNALGTVTTTGVLRKAE 1252

Qy   7556 RPSSSPCPDIGEVYADGVLLVWKPVESYGPVTYIVCSLEGGSWTTLASDIFDCCYLTSK 7615
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1253 RPSSSPCPDIGEVYADGVLLVWKPVESYGPVTYIVCSLEGGSWTTLASDIFDCCYLTSK 1312

Qy   7616 LSRGGTYTFRTACVSRAGMGPYSSPSEQVLIGGPSHLASEEESQGRSAQPLPSTKTFAFQ 7675
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1313 LSRGGTYTFRTACVSRAGMGPYSSPSEQVLIGGPSHLASEEESQGRSAQPLPSTKTFAFQ 1372

Qy   7676 TQIQRGRFSVVRQCWEKASGRALAAKIIPYHPKDKTAVLREYEALKGLRHPHLAQLHAAY 7735
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1373 TQIQRGRFSVVRQCWEKASGRALAAKIIPYHPKDKTAVLREYEALKGLRHPHLAQLHAAY 1432

Qy   7736 LSPRHLVLILELCSGPELLPCLAERASYSESEVKDYLWQMLSATQYLHNQHILHLDLRSE 7795
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1433 LSPRHLVLILELCSGPELLPCLAERASYSESEVKDYLWQMLSATQYLHNQHILHLDLRSE 1492

Qy   7796 NMIITEYNLLKVVDLGNAQSLSQEKVLPSDKFKDYLETMAPELLEGQGAVPQTDIWAIGV 7855
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Db   1493 NMIITEYNLLKVVDLGNAQSLSQEKVLPSDKFKDYLETMAPELLEGQGAVPQTDIWAIGV 1552
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Qy   7856 TAFIMLSAEYPVSSEGARDLQRGLRKGLVRLSRCYAGLSGGAVAFLRSTLCAQPWGRPCA 7915
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1553 TAFIMLSAEYPVSSEGARDLQRGLRKGLVRLSRCYAGLSGGAVAFLRSTLCAQPWGRPCA 1612

Qy   7916 SSCLQCPWLTEEGPACSRPAPVTFPTARLRVFVRNREKRALLYKRHNLAQVR 7968
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1613 SSCLQCPWLTEEGPACSRPAPVTFPTARLRVFVRNREKRALLYKRHNLAQVR 1665
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RESULT 2
US-10-274-978-2
; Sequence 2, Application US/1027 4978
; Patent No. 6670164
; GENERAL INFORMATION:
; APPLICANT: WEI, Ming-Hui, et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL000927-CIP-DIV
; CURRENT APPLICATION NUMBER: US/10/274,978
; CURRENT FILING DATE: 2002-10-22
; PRIOR APPLICATION NUMBER: 09/858,664
; PRIOR FILING DATE: 2001-05-17
; PRIOR APPLICATION NUMBER: 09/711,134
; PRIOR FILING DATE: 2000-11-14
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1665
; TYPE: PRT
; ORGANISM: Human
US-10-274-978-2

Query Match   20.4%; Score 8423; DB 4; Length 1665;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1612; Conservative 0; Mismatches 0; Indels 1; Gaps 0;

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Qy   6356 PPSMQVTIEDVQAQTGGTAQFEAIIEGDPQPSVTWYKDSVQLVDSTRLSQQEGTTYSLV 6415
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     53 PPSMQVTIEDVQAQTGGTAQFEAIIEGDPQPSVTWYKDSVQLVDSTRLSQQEGTTYSLV 112

Qy   6416 LRHVASKDAGVYTCLAQNTGGQVLCKAELLVLGGDNEPDSEKQSHRRKLHSFYEVKEBIG 6475
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    113 LRHVASKDAGVYTCLAQNTGGQVLCKAELLVLGGDNEPDSEKQSHRRKLHSFYEVKEBIG 172

Qy   6476 RGVFGFVRVQCHKGNKILCAAKFIPLRSRTRAQAYRERDIAALSHPLVTGLLDQFETRK 6535
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    173 RGVFGFVRVQCHKGNKILCAAKFIPLRSRTRAQAYRERDIAALSHPLVTGLLDQFETRK 232

Qy   6536 TLILLELCSSEELLDRLYRKGVVTEAEVKVYIQQLVEGLHYLHSHGVLHLDIKPSNILM 6595
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    233 TLILLELCSSEELLDRLYRKGVVTEAEVKVYIQQLVEGLHYLHSHGVLHLDIKPSNILM 292

Qy   6596 VHPAREDIKICDFGFAQNITPAELQFSQYGSPEFVSPEIIQQNPVSEASDIWAMGVISYL 6655
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    293 VHPAREDIKICDFGFAQNITPAELQFSQYGSPEFVSPEIIQQNPVSEASDIWAMGVISYL 352

Qy   6656 SLTCSSPFAGESDRATLLNVLEGRVSWNSSPMAAHLSEDAKDFIKATLQRAPQARPSAAQC 6715
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    353 SLTCSSPFAGESDRATLLNVLEGRVSWNSSPMAAHLSEDAKDFIKATLQRAPQARPSAAQC 412

Qy   6716 LSHPWFLKSMPAEEAHFINTKQLKFLLARSRWQRSLMSYKSILVMRSIPELLRGPPDSPS 6775
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    413 LSHPWFLKSMPAEEAHFINTKQLKFLLARSRWQRSLMSYKSILVMRSIPELLRGPPDSPS 472

Qy   6776 LGVARHLCRDTGGSSSSSSSSSSDNELAPFARAKSLPPSPVTHSPLLHPRGFLRPSASLPEE 6835
          ||||||||||||        ||||||||||||||||||||||||||||||||||||||||
Db    473 LGVARHLCRDTGGSSSSSSSSSSSSDNELAPFARAKSLPPSPVTHSPLLHPRGFLRPSASLPEE 532

Qy   6836 AEASERSTEAPAPPASPEGAGPPAAQGCVPRHSVIRSLFYHQAGESPEHGALAPGSRRHP 6895
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